PCT09

RAW SEQUENCE LISTING   DATE: 08/09/2001
PATENT APPLICATION: US/09/890,323   TIME: 12:04:10

Input Set : A:\2517-WO Seq.txt
Output Set: N:\CRF3\08092001\I890323.raw

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      3  <110> APPLICANT: Immunex Corporation
      5  <120> TITLE OF INVENTION: NEW METALLOPROTEINASE-DISINTEGRIN FAMILY MEMBERS: SVPH
      6         DNAS AND POLYPEPTIDES
      8  <130> FILE REFERENCE: 03260.0093-00304
C--> 10  <140> CURRENT APPLICATION NUMBER: US/09/890,323
C--> 11  <141> CURRENT FILING DATE: 2001-07-25
     13  <150> PRIOR APPLICATION NUMBER: 60/116,670
     14  <151> PRIOR FILING DATE: 1999-01-21
     16  <150> PRIOR APPLICATION NUMBER: 60/138,682
     17  <151> PRIOR FILING DATE: 1999-06-14
     19  <150> PRIOR APPLICATION NUMBER: 60/155,798
     20  <151> PRIOR FILING DATE: 1999-09-27
     22  <160> NUMBER OF SEQ ID NOS: 33
     24  <170> SOFTWARE: PatentIn Ver. 2.1
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     27  <211> LENGTH: 129
     28  <212> TYPE: DNA
     29  <213> ORGANISM: Homo sapiens
     31  <220> FEATURE:
     32  <223> OTHER INFORMATION: "n" at various positions throughout the sequence
     33         may be any nucleotide
     35  <400> SEQUENCE: 1
     36  atttttgata ccacagtgac caacacggtc acctaaggtg ttcaattctt tgtagcaagt 60
W--> 37  ctcacttgca gtatttgcgc ctgcaccaaa aatcctccta cactgttcan ttgcggtcat 120
W--> 38  gacangctc                                                          129
     41  <210> SEQ ID NO: 2
     42  <211> LENGTH: 469
     43  <212> TYPE: DNA
     44  <213> ORGANISM: Homo sapiens
     46  <400> SEQUENCE: 2
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     48  caacccagga ggacatgtga gtcacaatac cctttaatcc acaggttggc tccttggttt 120
     49  ctggaacttt ctgcctcctg taaacgatgt gcgggtggta ccctccctca accagtggat 180
     50  gcttcttcac gggttcaatg aaaaagtctc catgtggtag ttggaaaaat ccagtcagtc 240
     51  catggcaggc actgaggggt gccgtcccaa ctctggtgcc ctgctgtaga accgtgccac 300
     52  taagatggca gagggggca gaggaagcca tcatcttaac atgggagagg ttcccatatc 360
     53  tcttctccat gatgtagcta ttggaaagaa atccttcatt gaccgtcaag ttaaaaaaca 420
     54  aatccttctc ctcgtgagaa attctgtagt acacccagtc ctctgagcc            469
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     58  <211> LENGTH: 1500
     59  <212> TYPE: DNA
     60  <213> ORGANISM: Homo sapiens
     62  <400> SEQUENCE: 3
     63  cacgaggatt tatatcttca aagaaaatat aatgatgctc ttgcatggtc gtttggaaaa 60
     64  ...
```

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67 aattgcagtt atatctcttt ttttaaacat atctcttcgg gagcaacatg tctaaataat 300
68 atcccaggac taggttatgt gcttaagaga tgtggaaaca aaattgtgga ggacaatgag 360
69 gaatgtgatt gtggttccac agaggagtgt cagaaagatc ggtgttgcca atcaaattgt 420
70 aagttgcaac caggtgccaa ctgtagcatt ggactttgct gtcatgattg tcggtttcgt 480
71 ccatctggat acgtgtgtag gcaggaagga aatgaatgtg accttgcaga gtactgcgac 540
72 gggaattcaa gttcctgccc aaatgacgtt tataagcagg atggaacccc ttgcaagtat 600
73 gaaggccgtt gtttcaggaa ggggtgcaga tccagatata tgcagtgcca aagcattttt 660
74 ggacctgatg ccatggaggc tcctagtgag tgctatgatg cagttaactt aataggtgat 720
75 caatttggta actgtgagat tacaggaatt cgaaatttta aaaagtgtga aagtgcaaat 780
76 tcaatatgtg gcaggctaca gtgtataaat gttgaaacca tccctgattt gccagagcat 840
77 acgactataa tttctactca tttacaggca gaaaatctca tgtgctgggg cacaggctat 900
78 catctatcca tgaaacccat gggaatacct gacctaggta tgataaatga tggcacctcc 960
79 tgtggagaag gccgggtatg tttttaaaaaa aattgcgtca atagctcagt cctgcagttt 1020
80 gactgtttgc ctgagaaatg caatacccgg ggtgtttgca acaacagaaa aaactgccac 1080
81 tgcatgtatg ggtgggcacc tccattctgt gaggaagtgg ggtatggagg aagcattgac 1140
82 agtgggcctc caggactgct caggggggcg attccctcgt caatttgggt tgtgtccatc 1200
83 ataatgtttc gccttatttt attaatcctt tcagtggttt ttgtgttttt ccggcaagtg 1260
84 atagggaaacc acttaaaacc caaacaggaa aaaatgccac tatccaaagc aaaaactgaa 1320
85 caggaagaat ctaaaacaaa aactgtacag gaagaatcta aaacaaaaac tggacaggaa 1380
86 gaatctgaag caaaaactgg acaggaagaa tctaaagcaa aaactggaca ggaagaatct 1440
87 aaagcaaaca ttgaaagtaa acgacccaaa gcaaagagtg tcaagaaaca aaaaaagtaa 1500
90 <210> SEQ ID NO: 4
91 <211> LENGTH: 40
92 <212> TYPE: PRT
93 <213> ORGANISM: Homo sapiens
95 <220> FEATURE:
96 <223> OTHER INFORMATION: "Xaa" at various positions throughout the sequence
97       may be any amino acid
99 <400> SEQUENCE: 4
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W--> 100 **Met Thr Ala Xaa Glu Gln Cys Arg Arg Ile Phe Gly Ala Gly Ala Asn**
```
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103 Thr Ala Ser Glu Thr Cys Tyr Lys Glu Leu Asn Thr Leu Gly Asp Arg
104              20                  25                  30
106 Val Gly His Cys Gly Ile Lys Asn
107          35                  40
110 <210> SEQ ID NO: 5
111 <211> LENGTH: 123
112 <212> TYPE  PRT
113 <213> ORGANISM  Homo sapiens
115 <400> SEQUENCE: 5
116 Glu Asp Trp Val Tyr Tyr Arg Ile Ser His Glu Glu Lys Asp Leu Phe
117    1              5                   10                  15
119 Phe Asn Leu Thr Val Asn Glu Gly Phe Leu Ser Asn Ser Tyr Ile Met
120              20                  25                  30
122 Glu Lys Arg Tyr Gly Asn Leu Ser His Val Lys Met Met Ala Ser Ser
123          35                  40                  45
125 Ala Pro Leu Cys His Leu Ser Gly Thr Val Leu Gln Gln Gly Thr Arg
126      50                  55                  60
128 Val Gly Thr Ala Ala Leu Ser Ala Cys His ... ... ... ... ... ...
```

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129  65                    70                    75                    80
131 Gln Leu Pro His Gly Asp Phe Phe Ile Glu Pro Val Lys Lys His Pro
132              85                    90                    95
134 Leu Val Glu Gly Gly Tyr His Pro His Ile Val Tyr Arg Arg Gln Lys
135             100                   105                   110
137 Val Pro Glu Thr Lys Glu Pro Thr Cys Gly Leu
138          115                   120
141 <210> SEQ ID NO: 6
142 <211> LENGTH: 499
143 <212> TYPE: PRT
144 <213> ORGANISM: Homo sapiens
146 <400> SEQUENCE: 6
147 His Glu Asp Leu Tyr Leu Gln Arg Lys Tyr Asn Asp Ala Leu Ala Trp
148  1              5                    10                   15
150 Ser Phe Gly Lys Val Cys Ser Leu Glu Tyr Ala Gly Ser Val Ser Thr
151             20                    25                    30
153 Leu Leu Asp Thr Asn Ile Leu Ala Pro Ala Thr Trp Ser Ala His Glu
154          35                    40                    45
156 Leu Gly His Ala Val Gly Met Ser His Asp Glu Gln Tyr Cys Gln Cys
157       50                    55                    60
159 Arg Gly Arg Pro Asn Cys Ile Met Gly Ser Gly Arg Thr Gly Phe Ser
160  65                   70                    75                    80
162 Asn Cys Ser Tyr Ile Ser Phe Phe Lys His Ile Ser Ser Gly Ala Thr
163             85                    90                    95
165 Cys Leu Asn Asn Ile Pro Gly Leu Gly Tyr Val Leu Lys Arg Cys Gly
166             100                   105                   110
168 Asn Lys Ile Val Glu Asp Asn Glu Glu Cys Asp Cys Gly Ser Thr Glu
169          115                   120                   125
171 Glu Cys Gln Lys Asp Arg Cys Cys Gln Ser Asn Cys Lys Leu Gln Pro
172       130                   135                   140
174 Gly Ala Asn Cys Ser Ile Gly Leu Cys Cys His Asp Cys Arg Phe Arg
175 145                   150                   155                   160
177 Pro Ser Gly Tyr Val Cys Arg Gln Glu Gly Asn Glu Cys Asp Leu Ala
178             165                   170                   175
180 Glu Tyr Cys Asp Gly Asn Ser Ser Ser Cys Pro Asn Asp Val Tyr Lys
181          180                   185                   190
183 Gln Asp Gly Thr Pro Cys Lys Tyr Glu Gly Arg Cys Phe Arg Lys Gly
184          195                   200                   205
186 Cys Arg Ser Arg Tyr Met Gln Cys Gln Ser Ile Phe Gly Pro Asp Ala
187       210                   215                   220
189 Met Glu Ala Pro Ser Glu Cys Tyr Asp Ala Val Asn Leu Ile Gly Asp
190 225                   230                   235                   240
192 Gln Phe Gly Asn Cys Glu Ile Thr Gly Ile Arg Asn Phe Lys Lys Cys
193             245                   250                   255
195 Glu Ser Ala Asn Ser Ile Cys Gly Arg Leu Gln Cys Ile Asn Val Glu
196             260                   265                   270
198 Thr Ile Pro Asp Leu Pro Glu His Thr Thr Ile Ile Ser Thr His Leu
199          275                   280                   285
201 Gln Ala Glu Asn Leu Met Cys Trp Gly Thr Gly Tyr His Leu Gly Met
```

```
202     290                       295                     300
204 Lys Pro Met Gly Ile Pro Asp Leu Gly Met Ile Asn Asp Gly Thr Ser
205 305                310                    315                    320
207 Cys Gly Glu Gly Arg Val Cys Phe Lys Lys Asn Cys Val Asn Ser Ser
208                325                    330                    335
210 Val Leu Gln Phe Asp Cys Leu Pro Glu Lys Cys Asn Thr Arg Gly Val
211                340                    345                    350
213 Cys Asn Asn Arg Lys Asn Cys His Cys Met Tyr Gly Trp Ala Pro Pro
214                355                    360                    365
216 Phe Cys Glu Glu Val Gly Tyr Gly Gly Ser Ile Asp Ser Gly Pro Pro
217        370                    375                    380
219 Gly Leu Leu Arg Gly Ala Ile Pro Ser Ser Ile Trp Val Val Ser Ile
220 385                390                    395                    400
222 Ile Met Phe Arg Leu Ile Leu Leu Ile Leu Ser Val Val Phe Val Phe
223                405                    410                    415
225 Phe Arg Gln Val Ile Gly Asn His Leu Lys Pro Lys Gln Glu Lys Met
226                420                    425                    430
228 Pro Leu Ser Lys Ala Lys Thr Glu Gln Glu Glu Ser Lys Thr Lys Thr
229        435                    440                    445
231 Val Gln Glu Glu Ser Lys Thr Lys Thr Gly Gln Glu Glu Ser Glu Ala
232        450                    455                    460
234 Lys Thr Gly Gln Glu Glu Ser Lys Ala Lys Thr Gly Gln Glu Glu Ser
235 465                470                    475                    480
237 Lys Ala Asn Ile Glu Ser Lys Arg Pro Lys Ala Lys Ser Val Lys Lys
238                485                    490                    495
240 Gln Lys Lys
244 <210> SEQ ID NO: 7
245 <211> LENGTH: 2301
246 <212> TYPE: DNA
247 <213> ORGANISM: Homo sapiens
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251 caggatgagc acccccaata tcacagccct ccggatgtgg tgattcctgt gaggataact 120
252 ggcaccacca gaggcatgac acctccaggc tggctctcct atatcctgcc ctttggaggc 180
253 cagaaacaca ttatccacat aaaggtcaag aagctttttgt tttccaaaca cctccctgtg 240
254 ttcacctaca cagaccaggg tgctatcctt gaggaccagc catttgtcca gaataactgc 300
255 tactatcatg gttatgtgga aggggaccca gaatccctgg tttccctcag tacctgtttt 360
256 gggggttttc aaggaatatt acagataaat gactttgctt atgaaatcaa gcccctagca 420
257 tttttctacca cgtttgaaca tctggtatac aagatggaca gtgaggagaa acaatttttca 480
258 accatgagat ccggatttat gcaaaatgaa ataacatgcc gaatggaatt tgaagaaatt 540
259 gataattcca ctcagaagca aagttcttat gtgggctggt ggatccattt taggattgtt 600
260 gaaattgtag tcgtcattga taattatctg tacattcgtt atgaaaggaa cgactcaaag 660
261 ttgctggagg atctatatgt tattgttaat atagtggatt ccattttgga tgtcattggt 720
262 gttaaggtgt tattatttgg tttggagatc tggaccaata aaaacctcat tgtagtagat 780
263 gatgtaaggga aatctgtgca cctgtattgc aagtggaagt cggagaacat tacgccccgg 840
264 atgcaacatg acacctcaca tcttttcaca actctaggat taagagggtt aagtggcata 900
265 gggagctttta gaggaatgtg tacaccacac cgtagttgtg caattgttac tttcatgaac 960
266 aaaactttgg gcactttttc aattgcagtg gctcatcatc taggtcataa tttgggcatg 1020
267 aaccatgatg aggatacatg tcgttgttca caacctagat gcataatcgc ttt
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Input Set : **A:\2517-WO Seq.txt**
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268 ccaccaataa ctaaatttag caattgtagt tatggtgatt tttgggaata tactgtagag 1140
269 aggacaaagt gtttgcttga aacagtacac acaaaggaca tctttaatgt gaagcgctgt 1200
270 gggaatggtg ttgttgaaga aggagaagag tgtgactgtg gacctttaaa gcattgtgca 1260
271 aaagatccct gctgtctgtc aaattgcact ctgactgatg gttctacttg tgcttttggg 1320
272 ctttgttgca aagactgcaa gttcctacca tcagggaaag tgtgtagaaa ggaggtcaat 1380
273 gaatgtgatc ttccagagtg gtgcaatggt acttcccata agtgcccaga tgacttttat 1440
274 gtggaagatg gaattccctg taaggagagg ggctactgct atgaaaagag ctgtcatgac 1500
275 cgcaatgaac agtgtaggag gattttggt gcaggcgcaa atactgcaag tgagacttgc 1560
276 tacaaagaat tgaacacctt aggtgaccgt gttggtcact gtggtatcaa aaatgctaca 1620
277 tatataaagt gtaatatctc agatgtccag tgtggaagaa ttcagtgtga gaatgtgaca 1680
278 gaaattccca atatgagtga tcatactact gtgcattggg ctcgcttcaa tgacataatg 1740
279 tgctggagta ctgattacca tttggggatg aagggacctg atattggtga agtgaaagat 1800
280 ggaacagagt gtgggataga tcatatatgc atccacaggc actgtgtcca tataaccatc 1860
281 ttgaatagta attgctcacc tgcattttgt aacaagaggg gcatctgcaa caataaacat 1920
282 cactgccatt gcaattatct gtgggaccct cccaactgcc tgataaaagg ctatggaggt 1980
283 agtgttgaca gtggcccacc ccctaagaga aagaagaaaa agaagttctg ttatctgtgt 2040
284 atattgttgc ttattgtttt gtttattta ttatgttgtc tttatcgact ttgtaaaaaa 2100
285 agtaaaccaa taaaaaagca gcaagatgtt caaactccat ctgcaaaaga agaggaaaaa 2160
286 attcagcgtc gacctcatga gttacctccc cagagtcaac cttgggtgat gccttcccag 2220
287 agtcaacctc ctgtgacacc ctcccagagg caacctcagt tgatgccttc ccagagtcaa 2280
288 cctcctgtga cgccctccta g                                          2301
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292 <211> LENGTH: 2364
293 <212> TYPE: DNA
294 <213> ORGANISM: Homo sapiens
296 <400> SEQUENCE: 8
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298 caggatgagc accccaata tcacagccct ccggatgtgg tgattcctgt gaggataact 120
299 ggcaccacca gaggcatgac acctccaggc tggctctcct atatcctgcc ctttggaggc 180
300 cagaaacaca ttatccacat aaaggtcaag aagcttttgt tttccaaaca cctccctgtg 240
301 ttcacctaca cagaccaggg tgctatcctt gaggaccagc catttgtcca gaataactgc 300
302 tactatcatg gttatgtgga aggggaccca gaatccctgg tttccctcag tacctgtttt 360
303 gggggttttc aaggaatatt acagataaat gactttgctt atgaaatcaa gcccctagca 420
304 ttttctacca cgtttgaaca tctggtatac aagatggaca gtgaggagaa acaattttca 480
305 accatgagat ccggatttat gcaaaatgaa ataacatgcc gaatggaatt tgaagaaatt 540
306 gataattcca ctcagaagca aagttcttat gtgggctggt ggatccattt taggattgtt 600
307 gaaattgtag tcgtcattga taattatctg tacattcgtt atgaaaggaa cgactcaaag 660
308 ttgctggagg atctatatgt tattgttaat atagtggatt ccatttggga tgtcattggt 720
309 gttaaggtgt tattatttgg tttgggagatc tggaccaata aaaacctcat tgtagtagat 780
310 gatgtaagga aatctgtgca cctgtattgc aagtggaagt cggagaacat tacgcccagg 840
311 atgcaacatg acacctcaca tcttttcaca actctaggat taagagggtt aagtggcata 900
312 ggagctttta gaggaatgtg tacaccacac cgtagttgtg caattgttac tttcatgaac 960
313 aaaacttttgg gcactttttc aattgcagtg gctcatcatc taggtcataa tttgggcatg 1020
314 aaccatgatg aggatacatg tcgttgttca caacctagat gcataatgca tgaaggcaac 1080
315 ccaccaataa ctaaatttag caattgtagt tatggtgatt tttgggaata tactgtagag 1140
316 aggacaaagt gtttgcttga aacagtacac acaaaggaca tctttaatgt gaagcgctgt 1200
317 gggaatggtg ttgttgaaga aggagaagag tgtgactgtg gacctttaaa gcattgtgca 1260
318 aaagatccct gctgtctgtc aaattgcact ctgactgatg gttctacttg tgcttttggg 1320
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/890,323

DATE: 08/09/2001
TIME: 12:04:11

Input Set : **A:\2517-WO Seq.txt**
Output Set: **N:\CRF3\08092001\I890323.raw**

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L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:37 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:37 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:38 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:38 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:38 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:100 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:100 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:1471 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:31
L:1471 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:31
L:1471 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:31
L:1502 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:33
L:1502 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:33
L:1502 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
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